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Search Results -

Terms	Documents
20p1f12$	4

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Derwent World Patents Index
IBM Technical Disclosure Bulletins

Search: L2

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Search History

DATE: Thursday, August 22, 2002 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=OR			
L2	20p1f12$	4	L2
L1	$tmprss2	15	L1

END OF SEARCH HISTORY

```
=> file .gary
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                    85.27      85.48

FILE 'MEDLINE' ENTERED AT 18:30:42 ON 21 AUG 2002

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=> s ?tmprss2
L4          57 ?TMPRSS2

=> dup rem l4
PROCESSING COMPLETED FOR L4
L5          21 DUP REM L4 (36 DUPLICATES REMOVED)

=> s l5 and py<=1999
   2 FILES SEARCHED...
   3 FILES SEARCHED...
L6           3 L5 AND PY<=1999

=> d ibib abs 1-3

L6   ANSWER 1 OF 3     MEDLINE
ACCESSION NUMBER:   1999413460     MEDLINE
DOCUMENT NUMBER:    99413460   PubMed ID: 10485450
TITLE:              Prostate-localized and androgen-regulated expression of
the
                    membrane-bound serine protease TMPRSS2.
AUTHOR:             Lin B; Ferguson C; White J T; Wang S; Vessella R; True L
D;
                    Hood L; Nelson P S
CORPORATE SOURCE:   Department of Molecular Biotechnology, University of
                    Washington, Seattle 98195, USA.
CONTRACT NUMBER:    K08 CA75173-01A1 (NCI)
SOURCE:             CANCER RESEARCH, (1999 Sep 1) 59 (17) 4180-4.
                    Journal code: 2984705R. ISSN: 0008-5472.
PUB. COUNTRY:       United States
DOCUMENT TYPE:      Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
ENTRY MONTH:        199909
ENTRY DATE:         Entered STN: 19991012
                    Last Updated on STN: 20000303
                    Entered Medline: 19990930
AB   Genes regulated by androgenic hormones are of critical importance for the
     normal physiological function of the human prostate gland, and they
     contribute to the development and progression of prostate carcinoma. We
     used cDNA microarrays containing 1500 cDNAs to profile transcripts
     regulated by androgens in prostate cancer cells and identified the serine
     protease TMPRSS2 as a gene exhibiting increased expression upon
```

exposure to androgens. The **TMPRSS2** gene is located on chromosome 21 and contains four distinct domains, including a transmembrane region, indicating that it is expressed on the cell surface. Northern analysis demonstrated that **TMPRSS2** is highly expressed in prostate epithelium relative to other normal human tissues. In situ hybridization of normal and malignant prostate tissues localizes TMMPRSS2 expression to prostate basal cells and to prostate carcinoma. These results suggest that **TMPRSS2** may play a role in prostate carcinogenesis and should be investigated as a diagnostic or therapeutic target for the management of prostate cancers.

L6 ANSWER 2 OF 3 MEDLINE
ACCESSION NUMBER: 1999225676 MEDLINE
DOCUMENT NUMBER: 99225676 PubMed ID: 10207158
TITLE: A contiguous 3-Mb sequence-ready map in the S3-MX region on 21q22.2 based on high- throughput nonisotopic library screenings.
AUTHOR: Hildmann T; Kong X; O'Brien J; Riesselman L; Christensen H M; Dagand E; Lehrach H; Yaspo M L
CORPORATE SOURCE: Max Planck-Institut fur Molekulare Genetik, D-14195 Berlin-Dahlem, Germany.
SOURCE: GENOME RESEARCH, **(1999 Apr)** 9 (4) 360-72.
Journal code: 9518021. ISSN: 1088-9051.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990525
Last Updated on STN: 19990525
Entered Medline: 19990511

AB Progress in complete genomic sequencing of human chromosome 21 relies on the construction of high-quality bacterial clone maps spanning large chromosomal regions. To achieve this goal, we have applied a strategy based on nonradioactive hybridizations to contig building. A contiguous sequence-ready map was constructed in the Down syndrome congenital heart disease (DS-CHD) region in 21q22.2, as a framework for large-scale genomic sequencing and positional candidate gene approach. Contig assembly was performed essentially by high throughput nonisotopic screenings of genomic libraries, prior to clone validation by (1) restriction digest fingerprinting, (2) STS analysis, (3) Southern hybridizations, and (4) FISH analysis. The contig contains a total of 50 STSs, of which 13 were newly isolated. A minimum tiling path (MTP) was subsequently defined that consists of 20 PACs, 2 BACs, and 5 cosmids covering 3 Mb between D21S3 and MX1. Gene distribution in the region includes 9 known genes (c21-LRP, WRB, SH3BGR, HMG14, PCP4, DSCAM, MX2, MX1, and **TMPRSS2**) and 14 new additional gene signatures consisting of cDNA selection products and ESTs. Forthcoming genomic sequence information will unravel the structural organization of potential candidate genes involved in specific features of Down syndrome pathogenesis.

L6 ANSWER 3 OF 3 MEDLINE

ACCESSION NUMBER: 97468144 MEDLINE
DOCUMENT NUMBER: 97468144 PubMed ID: 9325052
TITLE: Cloning of the **TMPRSS2** gene, which encodes a novel serine protease with transmembrane, LDLRA, and SRCR domains and maps to 21q22.3.
COMMENT: Erratum in: Genomics 2001 Sep;77(1-2):114
AUTHOR: Paoloni-Giacobino A; Chen H; Peitsch M C; Rossier C; Antonarakis S E
CORPORATE SOURCE: Department of Genetics and Microbiology, Geneva University Medical School, Switzerland.
SOURCE: GENOMICS, **(1997 Sep 15)** 44 (3) 309-20.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U75329; GENBANK-X88043; GENBANK-X88047; GENBANK-X88228; GENBANK-X88229; GENBANK-X88321; PDB-1LDL
ENTRY MONTH: 199711
ENTRY DATE: Entered STN: 19971224
Last Updated on STN: 20000303
Entered Medline: 19971103

AB To contribute to the development of the transcription map of human chromosome 21 (HC21), we have used exon trapping from pools of HC21-specific cosmids. Using selected trapped exons, we have identified a novel gene (named **TMPRSS2**) that encodes a multimeric protein with a serine protease domain. The **TMPRSS2** 3.8-kb mRNA is expressed strongly in small intestine and weakly in several other tissues.

The full-length cDNA encodes a predicted protein of 492 amino acids that contains the following domains: (i) A serine protease domain (aa 255-492) of the S1 family that probably cleaves at Arg or Lys residues. (ii) An SRCR (scavenger receptor cysteine-rich) domain (aa 149-242) of group A (6 conserved Cys). This type of domain is involved in the binding to other cell surface or extracellular molecules. (iii) An LDLRA (LDL receptor class A) domain (aa 113-148). This type of domain forms a binding site for calcium. (iv) A predicted transmembrane domain (aa 84-106). No typical signal peptide was recognized. The gene was mapped to 21q22.3 between markers ERG and D21S56 in the same P1 as MX1. The physiological role of **TMPRSS2** and its involvement in trisomy 21 phenotypes or monogenic disorders that map to HC21 are unknown.

```
=> s 20p1f12?
L7            0 20P1F12?

=> s 2op1f12?
L8            0 2OP1F12?
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